

SEQUENCE LISTING

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KOIZUMI, SCHUICHI
KOHSAKA, SHINICHI
KOHSAKA, KAZUhide INOUE

<120> A SCREENING METHOD OF DRUG FOR TREATMENT OF NEUROPATHIC PAIN

<130> U 014843-4

<140> ---

<141> 2003-10-01

<160> 20

<170> PatentIn version 3.2

<210> 1

<211> 1167

<212> DNA

<213> HOMO SAPIENS

<220>

<221> CDS

<222> (1)..(1164)

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| Met Ala Gly Cys Cys Ser Ala Leu Ala Ala Phe Leu Phe Glu Tyr Asp | |
| 1 5 10 15 | |

| | |
|---|----|
| acg ccg cgc atc gtg ctc atc cgc agc cgc aaa gtg ggg ctc atg aac | 96 |
| Thr Pro Arg Ile Val Leu Ile Arg Ser Arg Lys Val Gly Leu Met Asn | |
| 20 25 30 | |

| | |
|---|-----|
| cgc gcc gtg caa ctg ctc atc ctg gcc tac gtc atc ggg tgg gtg ttt | 144 |
| Arg Ala Val Gln Leu Leu Ile Leu Ala Tyr Val Ile Gly Trp Val Phe | |
| 35 40 45 | |

| | |
|---|-----|
| gtg tgg gaa aag ggc tac cag gaa act gac tcc gtg gtc agc tcc gtt | 192 |
| Val Trp Glu Lys Gly Tyr Gln Glu Thr Asp Ser Val Val Ser Ser Val | |
| 50 55 60 | |

| | |
|---|-----|
| acg acc aag gtc aag ggc gtg gct gtg acc aac act tct aaa ctt gga | 240 |
| Thr Thr Lys Val Lys Gly Val Ala Val Thr Asn Thr Ser Lys Leu Gly | |
| 65 70 75 80 | |

| | |
|---|-----|
| ttc cgg atc tgg gat gtg gcg gat tat gtg ata cca gct cag gag gaa | 288 |
| Phe Arg Ile Trp Asp Val Ala Asp Tyr Val Ile Pro Ala Gln Glu Glu | |
| 85 90 95 | |

| | |
|---|-----|
| aac tcc ctc ttc gtc atg acc aac gtg atc ctc acc atg aac cag aca | 336 |
| Asn Ser Leu Phe Val Met Thr Asn Val Ile Leu Thr Met Asn Gln Thr | |
| 100 105 110 | |

| | |
|---|-----|
| cag ggc ctg tgc ccc gag att cca gat gcg acc act gtg tgt aaa tca | 384 |
| Gln Gly Leu Cys Pro Glu Ile Pro Asp Ala Thr Thr Val Cys Lys Ser | |
| 115 120 125 | |

| | |
|---|------|
| gat gcc agc tgt act gcc ggc tct gcc ggc acc cac agc aac gga gtc Asp Ala Ser Cys Thr Ala Gly Ser Ala Gly Thr His Ser Asn Gly Val 130 135 140 | 432 |
| tca aca ggc agg tgc gta gct ttc aac ggg tcc gtc aag acg tgt gag Ser Thr Gly Arg Cys Val Ala Phe Asn Gly Ser Val Lys Thr Cys Glu 145 150 155 160 | 480 |
| gtg gcg gcc tgg tgc ccg gtg gag gat gac aca cac gtg cca caa cct Val Ala Ala Trp Cys Pro Val Glu Asp Asp Thr His Val Pro Gln Pro 165 170 175 | 528 |
| gct ttt tta aag gct gca gaa aac ttc act ctt ttg gtt aag aac aac Ala Phe Leu Lys Ala Ala Glu Asn Phe Thr Leu Leu Val Lys Asn Asn 180 185 190 | 576 |
| atc tgg tat ccc aaa ttt aat ttc agc aag agg aat atc ctt ccc aac Ile Trp Tyr Pro Lys Phe Asn Phe Ser Lys Arg Asn Ile Leu Pro Asn 195 200 205 | 624 |
| atc acc act act tac ctc aag tcg tgc att tat gat gct aaa aca gat Ile Thr Thr Thr Tyr Leu Lys Ser Cys Ile Tyr Asp Ala Lys Thr Asp 210 215 220 | 672 |
| ccc ttc tgc ccc ata ttc cgt ctt ggc aaa ata gtg gag aac gca gga Pro Phe Cys Pro Ile Phe Arg Leu Gly Lys Ile Val Glu Asn Ala Gly 225 230 235 240 | 720 |
| cac agt ttc cag gac atg gcc gtg gag gga ggc atc atg ggc atc cag His Ser Phe Gln Asp Met Ala Val Glu Gly Gly Ile Met Gly Ile Gln 245 250 255 | 768 |
| gtc aac tgg gac tgc aac ctg gac aga gcc gcc tcc ctc tgc ttg ccc Val Asn Trp Asp Cys Asn Leu Asp Arg Ala Ala Ser Leu Cys Leu Pro 260 265 270 | 816 |
| agg tac tcc ttc cgc cgc ctc gat aca cgg gac gtt gag cac aac gta Arg Tyr Ser Phe Arg Arg Leu Asp Thr Arg Asp Val Glu His Asn Val 275 280 285 | 864 |
| tct cct ggc tac aat ttc agg ttt gcc aag tac tac aga gac ctg gct Ser Pro Gly Tyr Asn Phe Arg Phe Ala Lys Tyr Tyr Arg Asp Leu Ala 290 295 300 | 912 |
| ggc aac gag cag cgc acg ctc atc aag gcc tat ggc atc cgc ttc gac Gly Asn Glu Gln Arg Thr Leu Ile Lys Ala Tyr Gly Ile Arg Phe Asp 305 310 315 320 | 960 |
| atc att gtg ttt ggg aag gca ggg aaa ttt gac atc atc ccc act atg Ile Ile Val Phe Gly Lys Ala Gly Lys Phe Asp Ile Ile Pro Thr Met 325 330 335 | 1008 |
| atc aac atc ggc tct ggc ctg gca ctg cta ggc atg gcg acc gtg ctg Ile Asn Ile Gly Ser Gly Leu Ala Leu Leu Gly Met Ala Thr Val Leu 340 345 350 | 1056 |
| tgt gac atc ata gtc ctc tac tgc atg aag aaa aga ctc tac tat cgg Cys Asp Ile Ile Val Leu Tyr Cys Met Lys Lys Arg Leu Tyr Tyr Arg 355 360 365 | 1104 |
| gag aag aaa tat aaa tat gtg gaa gat tac gag cag ggt ctt gct agt | 1152 |

Glu Lys Lys Tyr Lys Tyr Val Glu Asp Tyr Glu Gln Gly Leu Ala Ser
 370 375 380

gag ctg gac cag tga
 Glu Leu Asp Gln
 385

1167

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Thr Pro Arg Ile Val Leu Ile Arg Ser Arg Lys Val Gly Leu Met Asn
 20 25 30

Arg Ala Val Gln Leu Leu Ile Leu Ala Tyr Val Ile Gly Trp Val Phe
 35 40 45

Val Trp Glu Lys Gly Tyr Gln Glu Thr Asp Ser Val Val Ser Ser Val
 50 55 60

Thr Thr Lys Val Lys Gly Val Ala Val Thr Asn Thr Ser Lys Leu Gly
 65 70 75 80

Phe Arg Ile Trp Asp Val Ala Asp Tyr Val Ile Pro Ala Gln Glu Glu
 85 90 95

Asn Ser Leu Phe Val Met Thr Asn Val Ile Leu Thr Met Asn Gln Thr
 100 105 110

Gln Gly Leu Cys Pro Glu Ile Pro Asp Ala Thr Thr Val Cys Lys Ser
 115 120 125

Asp Ala Ser Cys Thr Ala Gly Ser Ala Gly Thr His Ser Asn Gly Val
 130 135 140

Ser Thr Gly Arg Cys Val Ala Phe Asn Gly Ser Val Lys Thr Cys Glu
 145 150 155 160

Val Ala Ala Trp Cys Pro Val Glu Asp Asp Thr His Val Pro Gln Pro
 165 170 175

Ala Phe Leu Lys Ala Ala Glu Asn Phe Thr Leu Leu Val Lys Asn Asn
 180 185 190

Ile Trp Tyr Pro Lys Phe Asn Phe Ser Lys Arg Asn Ile Leu Pro Asn
195 200 205

Ile Thr Thr Thr Tyr Leu Lys Ser Cys Ile Tyr Asp Ala Lys Thr Asp
210 215 220

Pro Phe Cys Pro Ile Phe Arg Leu Gly Lys Ile Val Glu Asn Ala Gly
225 230 235 240

His Ser Phe Gln Asp Met Ala Val Glu Gly Gly Ile Met Gly Ile Gln
245 250 255

Val Asn Trp Asp Cys Asn Leu Asp Arg Ala Ala Ser Leu Cys Leu Pro
260 265 270

Arg Tyr Ser Phe Arg Arg Leu Asp Thr Arg Asp Val Glu His Asn Val
275 280 285

Ser Pro Gly Tyr Asn Phe Arg Phe Ala Lys Tyr Tyr Arg Asp Leu Ala
290 295 300

Gly Asn Glu Gln Arg Thr Leu Ile Lys Ala Tyr Gly Ile Arg Phe Asp
305 310 315 320

Ile Ile Val Phe Gly Lys Ala Gly Lys Phe Asp Ile Ile Pro Thr Met
325 330 335

Ile Asn Ile Gly Ser Gly Leu Ala Leu Leu Gly Met Ala Thr Val Leu
340 345 350

Cys Asp Ile Ile Val Leu Tyr Cys Met Lys Lys Arg Leu Tyr Tyr Arg
355 360 365

Glu Lys Lys Tyr Lys Tyr Val Glu Asp Tyr Glu Gln Gly Leu Ala Ser
370 375 380

Glu Leu Asp Gln
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<210> 3
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<220>
<223> Oligonucleotide

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|------------------------|--|----|
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| cagcccgccca tggctc | | 16 |
| <210> 4 | | |
| <211> 16 | | |
| <212> DNA | | |
| <213> ARTIFICIAL | | |
| <220> | | |
| <223> Oligonucleotide | | |
| <400> 4 | | |
| accgccgccca gtgcct | | 16 |
| <210> 5 | | |
| <211> 20 | | |
| <212> DNA | | |
| <213> ARTIFICIAL | | |
| <220> | | |
| <223> Primer | | |
| <400> 5 | | |
| tctttcttcgt gaggctgaga | | 20 |
| <210> 6 | | |
| <211> 20 | | |
| <212> DNA | | |
| <213> ARTIFICIAL | | |
| <220> | | |
| <223> Primer | | |
| <400> 6 | | |
| actggtagat gggtttgca | | 20 |
| <210> 7 | | |
| <211> 20 | | |
| <212> DNA | | |
| <213> ARTIFICIAL | | |
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| <400> 7 | | |
| gaatcagagt gcaaccccaa | | 20 |
| <210> 8 | | |
| <211> 20 | | |
| <212> DNA | | |
| <213> ARTIFICIAL | | |
| <220> | | |
| <223> Primer | | |

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| tcacaggcca tctacttgag | 20 |
| <210> 9 | |
| <211> 20 | |
| <212> DNA | |
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| <220> | |
| <223> Primer | |
| <400> 9 | |
| aagtaccgct gtgtgtctga | 20 |
| <210> 10 | |
| <211> 20 | |
| <212> DNA | |
| <213> ARTIFICIAL | |
| <220> | |
| <223> Primer | |
| <400> 10 | |
| atccagccga gtgaaggaat | 20 |
| <210> 11 | |
| <211> 20 | |
| <212> DNA | |
| <213> ARTIFICIAL | |
| <220> | |
| <223> Primer | |
| <400> 11 | |
| tcaccacgtc ctacctcaaa | 20 |
| <210> 12 | |
| <211> 20 | |
| <212> DNA | |
| <213> ARTIFICIAL | |
| <220> | |
| <223> Primer | |
| <400> 12 | |
| ctgctcgtag tcttccacat | 20 |
| <210> 13 | |
| <211> 20 | |
| <212> DNA | |
| <213> ARTIFICIAL | |
| <220> | |
| <223> Primer | |
| <400> 13 | |

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<210> 14
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taaggaactg gagaaacggc 20

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 tgc acc aga gac tac aaa atc acc cag gtc ctc ttc cca ctg ctc tac 96
 Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr
 20 25 30
 act gtc ctg ttt ttt gtt gga ctt atc aca aat ggc ctg gcg atg agg 144
 Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg
 35 40 45
 att ttc ttt caa atc cgg agt aaa tca aac ttt att att ttt ctt aag 192
 Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
 50 55 60
 aac aca gtc att tct gat ctt ctc atg att ctg act ttt cca ttc aaa 240
 Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
 65 70 75 80
 att ctt agt gat gcc aaa ctg gga aca gga cca ctg aga act ttt gtg 288
 Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
 85 90 95
 tgt caa gtt acc tcc gtc ata ttt tat ttc aca atg tat atc agt att 336
 Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
 100 105 110
 tca ttc ctg gga ctg ata act atc gat cgc tac cag aag acc acc agg 384
 Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg
 115 120 125
 cca ttt aaa aca tcc aac ccc aaa aat ctc ttg ggg gct aag att ctc 432
 Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
 130 135 140
 tct gtt gtc atc tgg gca ttc atg ttc tta ctc tct ttg cct aac atg 480
 Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
 145 150 155 160
 att ctg acc aac agg cag ccg aga gac aag aat gtg aag aaa tgc tct 528
 Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
 165 170 175
 ttc ctt aaa tca gag ttc ggt cta gtc tgg cat gaa ata gta aat tac 576
 Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr
 180 185 190

| | |
|---|------|
| atc tgt caa gtc att ttc tgg att aat ttc tta att gtt att gta tgt Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys 195 200 205 | 624 |
| tat aca ctc att aca aaa gaa ctg tac cgg tca tac gta aga acg agg Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg 210 215 220 | 672 |
| ggg gta ggt aaa gtc ccc agg aaa aag gtg aac gtc aaa gtt ttc att Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile 225 230 235 240 | 720 |
| atc att gct gta ttc ttt att tgt ttt gtt cct ttc cat ttt gcc cga Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg 245 250 255 | 768 |
| att cct tac acc ctg agc caa acc cgg gat gtc ttt gac tgc act gct Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala 260 265 270 | 816 |
| gaa aat act ctg ttc tat gtg aaa gag agc act ctg tgg tta act tcc Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser 275 280 285 | 864 |
| tta aat gca tgc ctg gat ccg ttc atc tat ttt ttc ctt tgc aag tcc Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser 290 295 300 | 912 |
| ttc aga aat tcc ttg ata agt atg ctg aag tgc ccc aat tct gca aca Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr 305 310 315 320 | 960 |
| tct ctg tcc cag gac aat agg aaa aaa gaa cag gat ggt ggt gac cca Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro 325 330 335 | 1008 |
| aat gaa gag act cca atg taa Asn Glu Glu Thr Pro Met 340 | 1029 |

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 <212> PRT
 <213> HOMO SAPIENS

<400> 20

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|--|

| |
|---|
| Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr 20 25 30 |
|---|

| |
|---|
| Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg 35 40 45 |
|---|

| |
|---|
| Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys |
|---|

50

55

60

Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
65 70 75 80

Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
85 90 95

Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
100 105 110

Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg
115 120 125

Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
130 135 140

Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
145 150 155 160

Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
165 170 175

Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr
180 185 190

Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys
195 200 205

Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg
210 215 220

Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile
225 230 235 240

Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg
245 250 255

Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala
260 265 270

Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser
275 280 285

Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser
290 295 300

Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr
305 310 315 320

Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro
325 330 335

- - - Asn Glu Glu Thr Pro Met
340